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gtt Val 95	cag Gln	aaa Lys	gta Val	aat Asn	gaa Glu 100	ata Ile	ggc Gly	att Ile	tac Tyr	ctg Leu 105	act Thr	gat Asp	tgc Cys	atg Met	gaa Glu 110	396
aga Arg	gct Ala	agg Arg	gaa Glu	gtg Val 115	att Ile	cca Pro	agg Arg	tcc Ser	cag Gln 120	cac His	caa Gln	gag Glu	aca Thr	ccc Pro 125	gtt Val	444
tac Tyr	ctg Leu	gga Gly	gcc Ala 130	acg Thr	gca Ala	ggc Gly	atg Met	cgg Arg 135	ttg Leu	ctc Leu	agg Arg	atg Met	gaa Glu 140	agt Ser	gaa Glu	492
gag Glu	ttg Leu 145	gca Ala	gac Asp	agg Arg	gtt Val	ctg Leu 150	gat Asp	gtg Val	gtg Val	gag Glu	agg Arg	agc Ser 155	ctc Leu	agc Ser	aac Asn	540
tac Tyr 160	ccc Pro	ttt Phe	gac Asp	ttc Phe	cag Gln	ggg Gly 165	gcc Ala	agg Arg	atc Ile	att Ile	act Thr 170	ggc Gly	caa Gln	gag Glu	gaa Glu	588
ggg Gly 175	gcc Ala	tat Tyr	ggc Gly	tgg Trp	att Ile 180	act Thr	atc Ile	aac Asn	tat Tyr	ctg Leu 185	ctg Leu	ggc Gly	aaa Lys	ttc Phe	agt Ser 190	636
cag Gln	aaa Lys	aca Thr	agg Arg	tgg Trp 195	ttc Phe	agc Ser	ata Ile	gtc Val	cca Pro 200	tat Tyr	gaa Glu	acc Thr	aat Asn	aat Asn 205	cag Gln	684
gaa Glu	acc Thr	ttt Phe	gga Gly 210	gct Ala	ttg Leu	gac Asp	ctt Leu	ggg Gly 215	gga Gly	gcc Ala	tct Ser	aca Thr	caa Gln 220	gtc Val	act Thr	732
ttt Phe	gta Val 225	ccc Pro	caa Gln	aac Asn	cag Gln	act Thr	atc Ile 230	gag Glu	tcc Ser	cca Pro	gat Asp 235	aat Asn	gct Ala	ctg Leu	caa Gln	780
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tgc Cys 255	tat Tyr	ggg Gly	aag Lys	gat Asp	cag Gln 260	gca Ala	ctc Leu	tgg Trp	cag Gln	aaa Lys 265	ctg Leu	gcc Ala	aag Lys	gac Asp	att Ile 270	876
cag Gln	gtt Val	gca Ala	agt Ser	aat Asn 275	gaa Glu	att Ile	ctc Leu	agg Arg	gac Asp 280	cca Pro	tgc Cys	ttt Phe	cat His	cct Pro 285	gga Gly	924
tat Tyr	aag Lys	aag Lys	gta Val 290	gtg Val	aac Asn	gta Val	agt Ser	gac Asp 295	ctt Leu	tac Tyr	aag Lys	acc Thr	ccc Pro 300	tgc Cys	acc Thr	972
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Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val	
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Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys	
385 390 395	
aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt	1308
Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe	
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tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca	1356
Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr	
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Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser	
435 440 445	
gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc	1452
Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile	
450 455 460	
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Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val	
465 470 475	
ttc ctc atg gtt cta ttc tcc ctg gtc ctt ttc aca gtg gcc atc ata	1548
Phe Leu Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile	
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ggc ttg ctt atc ttt cac aag cct tca tat ttc tgg aaa gat atg gta	1596
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 355 360 365
 Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
 370 375 380
 Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
 385 390 395 400
 Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
 405 410 415
 Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
 420 425 430
 Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
 435 440 445
 Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
 450 455 460
 Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu
 465 470 475 480
 Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu
 485 490 495
 Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val
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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Fusion
construct of human CD39

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 Ile Phe Leu Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
 35 40 45
 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
 50 55 60
 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
 65 70 75 80
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95

Lys	Val	Asn	Glu 100	Ile	Gly	Ile	Tyr	Leu 105	Thr	Asp	Cys	Met	Glu 110	Arg	Ala
Arg	Glu	Val 115	Ile	Pro	Arg	Ser	Gln 120	His	Gln	Glu	Thr	Pro 125	Val	Tyr	Leu
Gly	Ala	Thr	Ala	Gly	Met	Arg 135	Leu	Leu	Arg	Met	Glu 140	Ser	Glu	Glu	Leu
Ala 145	Asp	Arg	Val	Leu	Asp 150	Val	Val	Glu	Arg	Ser 155	Leu	Ser	Asn	Tyr	Pro 160
Phe	Asp	Phe	Gln 165	Gly	Ala	Arg	Ile	Ile 170	Thr	Gly	Gln	Glu	Glu	Gly 175	Ala
Tyr	Gly	Trp	Ile 180	Thr	Ile	Asn	Tyr	Leu 185	Leu	Gly	Lys	Phe	Ser 190	Gln	Lys
Thr	Arg	Trp 195	Phe	Ser	Ile	Val	Pro 200	Tyr	Glu	Thr	Asn 205	Asn	Gln	Glu	Thr
Phe	Gly 210	Ala	Leu	Asp	Leu	Gly 215	Gly	Ala	Ser	Thr	Gln 220	Val	Thr	Phe	Val
Pro 225	Gln	Asn	Gln	Thr 230	Ile	Glu	Ser	Pro	Asp	Asn 235	Ala	Leu	Gln	Phe	Arg 240
Leu	Tyr	Gly	Lys 245	Asp	Tyr	Asn	Val	Tyr	Thr 250	His	Ser	Phe	Leu	Cys 255	Tyr
Gly	Lys	Asp	Gln 260	Ala	Leu	Trp	Gln	Lys 265	Leu	Ala	Lys	Asp	Ile 270	Gln	Val
Ala	Ser	Asn 275	Glu	Ile	Leu	Arg	Asp 280	Pro	Cys	Phe	His	Pro 285	Gly	Tyr	Lys
Lys	Val 290	Val	Asn	Val	Ser	Asp 295	Leu	Tyr	Lys	Thr	Pro 300	Cys	Thr	Lys	Arg
Phe 305	Glu	Met	Thr	Leu	Pro 310	Phe	Gln	Gln	Phe	Glu 315	Ile	Gln	Gly	Ile	Gly 320
Asn	Tyr	Gln	Gln	Cys 325	His	Gln	Ser	Ile	Leu 330	Glu	Leu	Phe	Asn	Thr 335	Ser
Tyr	Cys	Pro	Tyr 340	Ser	Gln	Cys	Ala	Phe 345	Asn	Gly	Ile	Phe	Leu 350	Pro	Pro
Leu	Gln	Gly 355	Asp	Phe	Gly	Ala	Phe 360	Ser	Ala	Phe	Tyr	Phe 365	Val	Met	Lys
Phe	Leu 370	Asn	Leu	Thr	Ser	Glu 375	Lys	Val	Ser	Gln	Glu 380	Lys	Val	Thr	Glu
Met 385	Met	Lys	Lys	Phe	Cys 390	Ala	Gln	Pro	Trp	Glu 395	Glu	Ile	Lys	Thr	Ser 400
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Gln	Asn	Lys	Ala	Leu	Pro	Glu	Asn	Val	Lys	Tyr	Gly	Ile	Val	Leu	Asp		
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Ala	Gly	Ser	Ser	His	Thr	Ser	Leu	Tyr	Ile	Tyr	Lys	Trp	Pro	Ala	Glu		
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aag	gag	aat	gac	aca	ggc	gtg	gtg	cat	caa	gta	gaa	gaa	tgc	agg	gtt		192
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Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	Arg	Ala	Arg	Glu	Val	Ile	Pro	Arg		
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tcc	cag	cac	caa	gag	aca	ccc	gtt	tac	ctg	gga	gcc	acg	gca	ggc	atg		336
Ser	Gln	His	Gln	Glu	Thr	Pro	Val	Tyr	Leu	Gly	Ala	Thr	Ala	Gly	Met		
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Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	Tyr	Pro	Phe	Asp	Phe	Gln	Gly	Ala		
	130					135					140						
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Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	Gly	Ala	Tyr	Gly	Trp	Ile	Thr	Ile		
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gac Asp	ctt Leu	tac Tyr 275	aag Lys	acc Thr	ccc Pro	tgc Cys	acc Thr 280	aag Lys	aga Arg	ttt Phe	gag Glu	atg Met 285	act Thr	ctt Leu	cca Pro	864
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tgt Cys	gcc Ala	ttc Phe	aat Asn	ggg Gly 325	att Ile	ttc Phe	ttg Leu	cca Pro	cca Pro 330	ctc Leu	cag Gln	ggg Gly	gat Asp	ttt Phe 335	ggg Gly	1008
gca Ala	ttt Phe	tca Ser	gct Ala 340	ttt Phe	tac Tyr	ttt Phe	gtg Val 345	atg Met	aag Lys	ttt Phe	tta Leu	aac Asn	ttg Leu 350	aca Thr	tca Ser	1056
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aag Lys 385	tac Tyr	ctg Leu	agt Ser	gaa Glu	tac Tyr 390	tgc Cys	ttt Phe	tct Ser	ggg Gly	acc Thr 395	tac Tyr	att Ile	ctc Leu	tcc Ser	ctc Leu 400	1200
ctt Leu	ctg Leu	caa Gln	ggc Gly	tat Tyr 405	cat His	ttc Phe	aca Thr	gct Ala	gat Asp 410	tcc Ser	tgg Trp	gag Glu	cac His	atc Ile 415	cat His	1248
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Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys	
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aaa aca cag cta act agt tca acc cag aac aaa gca ttg cca gaa aac	144
Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn	
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Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu	
50 55 60	
tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg	240
Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val	
65 70 75 80	
cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt	288
His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe	
85 90 95	
gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa	336
Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu	
100 105 110	
aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt	384
Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val	
115 120 125	
tac ctg gga gcc acg gca ggc atg cgg ttg ctc agg atg gaa agt gaa	432
Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu	
130 135 140	
gag ttg gca gac agg gtt ctg gat gtg gtg gag agg agc ctc agc aac	480
Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn	
145 150 155 160	
tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa	528
Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu	
165 170 175	
ggg gcc tat ggc tgg att act atc aac tat ctg ctg ggc aaa ttc agt	576
Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser	
180 185 190	
cag aaa aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag	624
Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln	
195 200 205	
gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act	672
Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr	
210 215 220	

ttt Phe 225	gta Val	ccc Pro	caa Gln	aac Asn	cag Gln 230	act Thr	atc Ile	gag Glu	tcc Ser	cca Pro 235	gat Asp	aat Asn	gct Ala	ctg Leu	caa Gln 240	720
ttt Phe	cgc Arg	ctc Leu	tat Tyr	ggc Gly 245	aag Lys	gac Asp	tac Tyr	aat Asn	gtc Val 250	tac Tyr	aca Thr	cat His	agc Ser	ttc Phe 255	ttg Leu	768
tgc Cys	tat Tyr	ggg Gly	aag Lys 260	gat Asp	cag Gln	gca Ala	ctc Leu	tgg Trp 265	cag Gln	aaa Lys	ctg Leu	gcc Ala	aag Lys 270	gac Asp	att Ile	816
cag Gln	gtt Val	gca Ala 275	agt Ser	aat Asn	gaa Glu	att Ile	ctc Leu 280	agg Arg	gac Asp	cca Pro	tgc Cys	ttt Phe 285	cat His	cct Pro	gga Gly	864
tat Tyr	aag Lys 290	aag Lys	gta Val	gtg Val	aac Asn	gta Val 295	agt Ser	gac Asp	ctt Leu	tac Tyr	aag Lys 300	acc Thr	ccc Pro	tgc Cys	acc Thr	912
aag Lys 305	aga Arg	ttt Phe	gag Glu	atg Met	act Thr 310	ctt Leu	cca Pro	ttc Phe	cag Gln	cag Gln 315	ttt Phe	gaa Glu	atc Ile	cag Gln	ggc Gly 320	960
att Ile	gga Gly	aac Asn	tat Tyr	caa Gln 325	caa Gln	tgc Cys	cat His	caa Gln	agc Ser 330	atc Ile	ctg Leu	gag Glu	ctc Leu	ttc Phe 335	aac Asn	1008
acc Thr	agt Ser	tac Tyr	tgc Cys 340	cct Pro	tac Tyr	tcc Ser	cag Gln	tgt Cys 345	gcc Ala	ttc Phe	aat Asn	ggg Gly	att Ile 350	ttc Phe	ttg Leu	1056
cca Pro	cca Pro	ctc Leu 355	cag Gln	ggg Gly	gat Asp	ttt Phe	ggg Gly 360	gca Ala	ttt Phe	tca Ser	gct Ala	ttt Phe 365	tac Tyr	ttt Phe	gtg Val	1104
atg Met	aag Lys 370	ttt Phe	tta Leu	aac Asn	ttg Leu	aca Thr 375	tca Ser	gag Glu	aaa Lys	gtc Val	tct Ser	cag Gln	gaa Glu	aag Lys	gtg Val	1152
act Thr 385	gag Glu	atg Met	atg Met	aaa Lys	aag Lys 390	ttc Phe	tgt Cys	gct Ala	cag Gln	cct Pro 395	tgg Trp	gag Glu	gag Glu	ata Ile	aaa Lys 400	1200
aca Thr	tct Ser	tac Tyr	gct Ala 405	gga Gly	gta Val	aag Lys	gag Glu	aag Lys	tac Tyr 410	ctg Leu	agt Ser	gaa Glu	tac Tyr	tgc Cys 415	ttt Phe	1248
tct Ser	ggc Gly	acc Thr	tac Tyr 420	att Ile	ctc Leu	tcc Ser	ctc Leu	ctt Leu 425	ctg Leu	caa Gln	ggc Gly	tat Tyr	cat His 430	ttc Phe	aca Thr	1296
gct Ala	gat Asp	tcc Ser 435	tgg Trp	gag Glu	cac His	atc Ile	cat His 440	ttc Phe	att Ile	ggc Gly	aag Lys	atc Ile 445	cag Gln	ggc Gly	agc Ser	1344
gac Asp	gcc Ala 450	ggc Gly	tgg Trp	act Thr	ttg Leu	ggc Gly 455	tac Tyr	atg Met	ctg Leu	aac Asn	ctg Leu 460	acc Thr	aac Asn	atg Met	atc Ile	1392

Phe	Arg	Leu	Tyr	Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu
				245					250					255	
Cys	Tyr	Gly	Lys	Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile
			260					265					270		
Gln	Val	Ala	Ser	Asn	Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly
		275					280					285			
Tyr	Lys	Lys	Val	Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr
	290					295					300				
Lys	Arg	Phe	Glu	Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly
305					310					315					320
Ile	Gly	Asn	Tyr	Gln	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn
				325					330					335	
Thr	Ser	Tyr	Cys	Pro	Tyr	Ser	Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu
			340					345					350		
Pro	Pro	Leu	Gln	Gly	Asp	Phe	Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val
		355					360					365			
Met	Lys	Phe	Leu	Asn	Leu	Thr	Ser	Glu	Lys	Val	Ser	Gln	Glu	Lys	Val
	370					375					380				
Thr	Glu	Met	Met	Lys	Lys	Phe	Cys	Ala	Gln	Pro	Trp	Glu	Glu	Ile	Lys
385					390					395					400
Thr	Ser	Tyr	Ala	Gly	Val	Lys	Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe
				405					410					415	
Ser	Gly	Thr	Tyr	Ile	Leu	Ser	Leu	Leu	Leu	Gln	Gly	Tyr	His	Phe	Thr
			420					425					430		
Ala	Asp	Ser	Trp	Glu	His	Ile	His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser
		435					440					445			
Asp	Ala	Gly	Trp	Thr	Leu	Gly	Tyr	Met	Leu	Asn	Leu	Thr	Asn	Met	Ile
	450					455					460				
Pro	Ala	Glu	Gln	Pro	Leu	Ser	Thr	Pro	Leu	Ser	His	Ser	Thr		
465					470					475					

<210> 9

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
signal sequence

<400> 9

Met	Ala	Leu	Trp	Ile	Asp	Arg	Met	Gln	Leu	Leu	Ser	Cys	Ile	Ala	Leu
1					5				10					15	

Ser Leu Ala Leu Val Thr Asn Ser

<210> 10
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 10
 Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 11
 <211> 43
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 11
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
 20 25 30

Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys
 35 40

<210> 12
 <211> 29
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 12
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys
 20 25

<210> 13
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 13

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Ser Thr Gln Asn Lys
20 25 30

<210> 14

<211> 87

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 14

cgggctggac ttggtggtac atgctgaacc tgaccaacat gatcccagct gagcaaccat 60

tgtccacacc tctctcccac gagcccc 87

<210> 15

<211> 87

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 15

gatcggggct cgtgggagag aggtgtggac aatgggttgct cagctgggat catgttggtc 60

aggttcagca tgtagcccaa agtccag 87

<210> 16

<211> 740

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (42)..(737)

<400> 16

cgtaccgct agcgtcgaca ggcctaggat atcgatacgt a gag ccc aga tct tgt 56
Glu Pro Arg Ser Cys
1 5

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc gag ggc 104
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly
10 15 20

[illegible]

Glu Pro Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg
145 150 155 160

His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<211> 18

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 18

ctttccatcc tgagcaac

18

<210> 19

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 19

aaaaaactag tcagaacaaa gctttgccag aaaacg

36

<210> 20

<211> 24

<212> PRT

<213> Mus sp.

<400> 20

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
1 5 10 15

Leu Val Leu Leu Pro Val Thr Ser
20

<210> 21

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 21

ctagttctgg agactacaaa gatgacgatg acaaaaccga gaacaa

46

<210> 22

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 22

agctttgttc tgggttttgc catcgatc tttgtagtct ccagaa

46

<210> 23

<211> 89

<212> DNA

<213> Artificial Sequence

[illegible]

<400> 23

<210> 24

<211> 89

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 24

<210> 25

<211> 1464

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1) . . (1461)

<220>

<223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 25

atg gcc ctg tgg atc gac agg atg caa ctc ctg tct tgc att gca cta 48
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag 96
 Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
 20 25 30

aaa aca cag cta act agt tca gga gac tac aaa gat gac gat gac aaa 144
Lys Thr Gln Leu Thr Ser Ser Gly Asp Tyr Lys Asp Asp Asp Asp Lys
35 40 45

acc cag aac aaa gca ttg cca gaa aac gtt aag tat ggg att gtg ctg 192
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
50 55 60

gat gcg ggt tct tct cac aca agt tta tac atc tat aag tgg cca gca 240
Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
65 70 75 80

gaa aag gag aat gac aca ggc gtg gtg cat caa gta gaa gaa tgc agg 288

Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	Ile	Gly	Asn	Tyr	Gln	Gln	Cys	
				325					330					335		
cat	caa	agc	atc	ctg	gag	ctc	ttc	aac	acc	agt	tac	tgc	cct	tac	tcc	1056
His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	Thr	Ser	Tyr	Cys	Pro	Tyr	Ser	
			340					345					350			
cag	tgt	gcc	ttc	aat	ggg	att	ttc	ttg	cca	cca	ctc	cag	ggg	gat	ttt	1104
Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu	Pro	Pro	Leu	Gln	Gly	Asp	Phe	
		355					360					365				
ggg	gca	ttt	tca	gct	ttt	tac	ttt	gtg	atg	aag	ttt	tta	aac	ttg	aca	1152
Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val	Met	Lys	Phe	Leu	Asn	Leu	Thr	
	370					375					380					
tca	gag	aaa	gtc	tct	cag	gaa	aag	gtg	act	gag	atg	atg	aaa	aag	ttc	1200
Ser	Glu	Lys	Val	Ser	Gln	Glu	Lys	Val	Thr	Glu	Met	Met	Lys	Lys	Phe	
	385				390					395					400	
tgt	gct	cag	cct	tgg	gag	gag	ata	aaa	aca	tct	tac	gct	gga	gta	aag	1248
Cys	Ala	Gln	Pro	Trp	Glu	Glu	Ile	Lys	Thr	Ser	Tyr	Ala	Gly	Val	Lys	
				405					410					415		
gag	aag	tac	ctg	agt	gaa	tac	tgc	ttt	tct	ggt	acc	tac	att	ctc	tcc	1296
Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe	Ser	Gly	Thr	Tyr	Ile	Leu	Ser	
			420					425					430			
ctc	ctt	ctg	caa	ggc	tat	cat	ttc	aca	gct	gat	tcc	tgg	gag	cac	atc	1344
Leu	Leu	Leu	Gln	Gly	Tyr	His	Phe	Thr	Ala	Asp	Ser	Trp	Glu	His	Ile	
			435				440					445				
cat	ttc	att	ggc	aag	atc	cag	ggc	agc	gac	gcc	ggc	tgg	act	ttg	ggc	1392
His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser	Asp	Ala	Gly	Trp	Thr	Leu	Gly	
	450					455					460					
tac	atg	ctg	aac	ctg	acc	aac	atg	atc	cca	gct	gag	caa	cca	ttg	tcc	1440
Tyr	Met	Leu	Asn	Leu	Thr	Asn	Met	Ile	Pro	Ala	Glu	Gln	Pro	Leu	Ser	
	465				470				475						480	
aca	cct	ctc	tcc	cac	tcc	acc	taa									1464
Thr	Pro	Leu	Ser	His	Ser	Thr										
				485												

<210> 26
 <211> 487
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion
 construct of human CD39

<400> 26
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15
 Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
 20 25 30

Lys Thr Gln Leu Thr Ser Ser Gly Asp Tyr Lys Asp Asp Asp Asp Lys
 35 40 45
 Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
 50 55 60
 Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
 65 70 75 80
 Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
 85 90 95
 Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
 100 105 110
 Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
 115 120 125
 Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
 130 135 140
 Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu
 145 150 155 160
 Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
 165 170 175
 Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
 180 185 190
 Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser
 195 200 205
 Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp
 210 215 220
 Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr
 225 230 235 240
 Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp
 245 250 255
 Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala
 260 265 270
 Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile
 275 280 285
 Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val
 290 295 300
 Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu
 305 310 315 320
 Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys
 325 330 335
 His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser
 340 345 350

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210	215	220
Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr 225 230 235 240		
Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys 245 250 255		
Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser 260 265 270		
Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val 275 280 285		
Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu 290 295 300		
Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr 305 310 315 320		
Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys 325 330 335		
Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln 340 345 350		
Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu 355 360 365		
Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met 370 375 380		
Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala 385 390 395 400		
Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr 405 410 415		
Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp 420 425 430		
Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp 435 440 445		
Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln 450 455 460		
Pro Leu Ser Thr Pro Leu Ser His Ser Thr 465 470		

<210> 29

<211> 473

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

[illegible]

Met	Ala	Leu	Trp	Ile	Asp	Arg	Met	Gln	Leu	Ser	Cys	Ile	Ala	Leu	
1				5				10					15		
Ser	Leu	Ala	Leu	Val	Thr	Asn	Ser	Ser	Thr	Lys	Lys	Thr	Gln	Leu	Thr
			20					25					30		
Ser	Ser	Thr	Gln	Asn	Lys	Ala	Leu	Pro	Glu	Asn	Val	Lys	Tyr	Gly	Ile
		35					40					45			
Val	Leu	Asp	Ala	Gly	Ser	Ser	His	Thr	Ser	Leu	Tyr	Ile	Tyr	Lys	Trp
	50					55					60				
Pro	Ala	Glu	Lys	Glu	Asn	Asp	Thr	Gly	Val	Val	His	Gln	Val	Glu	Glu
65					70					75					80
Cys	Arg	Val	Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe	Val	Gln	Lys	Val	Asn
				85					90					95	
Glu	Ile	Gly	Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	Arg	Ala	Arg	Glu	Val
			100					105					110		
Ile	Pro	Arg	Ser	Gln	His	Gln	Glu	Thr	Pro	Val	Tyr	Leu	Gly	Ala	Thr
		115					120					125			
Ala	Gly	Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	Glu	Leu	Ala	Asp	Arg
	130					135					140				
Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	Tyr	Pro	Phe	Asp	Phe
145					150					155					160
Gln	Gly	Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	Gly	Ala	Tyr	Gly	Trp
				165				170						175	
Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	Gln	Lys	Thr	Arg	Trp
			180					185					190		
Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	Glu	Thr	Phe	Gly	Ala
		195					200					205			
Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	Phe	Val	Pro	Gln	Asn
	210					215					220				
Gln	Thr	Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	Phe	Arg	Leu	Tyr	Gly
225					230					235					240
Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	Cys	Tyr	Gly	Lys	Asp
				245					250					255	
Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	Gln	Val	Ala	Ser	Asn
			260					265					270		
Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	Tyr	Lys	Lys	Val	Val
		275					280					285			
Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	Lys	Arg	Phe	Glu	Met
	290					295					300				
Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	Ile	Gly	Asn	Tyr	Gln

